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NETAFFX™ ANALYSIS CENTER

Details for HG-U95AV2:36809_AT

Full Screen

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GeneChip Array Information

Probe Set ID	36809_at
GeneChip Array	Human Genome U95Av2 Array
Organism	Human
Common Name	




Probe Design Information

Transcript ID (Array Design)	4849545
Sequence Type	Consensus sequence
Representative Public ID	L01664 NCBI
Archival UniGene Cluster	Hs.889 NCBI
Target Description	Cluster Incl. L01664:Human eosinophil Charcot-Leyden crystal (CLC) protein (lysophospholipase) mRNA, complete cds /cds=(33,461) /gb=L01664 /gi=187273 /ug=Hs.889 /len=586

Annotation Method Description

Annotation Description	36809_at was annotated using the Matching Probes based pipeline to a Entrez Gene identifier using 6 transcript(s).
Annotation Grade	This is a grade A annotation.
Annotation Transcript Cluster (# of Matching Probes)	BC119711(16), BC119712(16), ENST00000221804(15), ENST00000392050(14), L01664(16), NM_001828(15)

	Representative Transcript	Description	Matching Probes	Related Probesets by Grade
Transcript Assignments	BC119711 NCBI	Homo sapiens Charcot-Leyden crystal protein, mRNA (cDNA clone MGC:149659 IMAGE:40117193), complete cds.	16/16	None
	BC119712 NCBI	Homo sapiens Charcot-Leyden crystal protein, mRNA (cDNA clone MGC:149660 IMAGE:40117194), complete cds.	16/16	None
	ENST00000221804 Ensembl	Eosinophil lysophospholipase gene: ENSG00000105205	15/16	None
	ENST00000392050 Ensembl	Uncharacterized protein CLC (Fragment) gene: ENSG00000105205	14/16	None

	GENSCAN00000021246 Ensembl	cdna:Genscan chromosome: NCBI36:19:44908625:44920939:-1	13/16	None
	L01664 NCBI	Homo sapiens Charcot-Leyden crystal protein mRNA, complete cds.	16/16	None
	NM_001828 NCBI	Homo sapiens Charcot-Leyden crystal protein (CLC), mRNA.	15/16	None
	uc002omh.1 UCSC		15/16	None
Annotation Notes	There are no noteworthy cross hybridizing mRNAs found for this probe set.			
Genomic Alignment of Consensus/Exemplar Sequence 				
Assembly	March 2006 (NCBI Build 36.1)			
Alignment(s)	Position	View using IGB	Identity	Coverage
	chr19:44913857-44917553(-) UCSC ENSEMBL	IGB *	88.84	88.8
* You can now view alignments using the Integrated Genome Browser (IGB) . Note that you must start IGB before clicking on any of the "IGB" links above.				
Public Domain and Genome References 				
Gene Title	Charcot-Leyden crystal protein			
Gene Symbol	CLC HGNC			
Chromosomal Location	19q13.1			
UniGene ID	Hs.889 NCBI (FULL LENGTH)			
Build 212 (11 Apr 2008)				
Ensembl	ENSG00000105205			
Entrez Gene ID	1178 Entrez gene			
SwissProt	A8MXT7 EMBL-EBI Q05315 EMBL-EBI			
EC	3.1.1.5			
OMIM	153310 NCBI			
RefSeq Protein ID	NP_001819.2 NCBI			
RefSeq	RefSeq Transcript ID RefSeq Title NM_001828 NCBI			
Functional Annotations 				
Gene Ontology	GO Biological Process (view graph)			
	ID	Description	Evidence	Links
	0006644	phospholipid metabolic process	not recorded	QuickGO AmiGO
	0007275	multicellular organismal development	traceable author statement	QuickGO AmiGO
	0016042	lipid catabolic process	inferred from electronic annotation	QuickGO AmiGO
	GO Molecular Function (view graph)			
	ID	Description	Evidence	Links
	0004091	carboxylesterase activity	inferred from electronic annotation	QuickGO AmiGO
	0004622	lysophospholipase activity	inferred from electronic annotation	QuickGO AmiGO
	0005529	sugar binding	inferred from electronic annotation	QuickGO AmiGO
	0016787	hydrolase activity	inferred from electronic annotation	QuickGO AmiGO

>HG-U95AV2:36809_AT

[illegible]

BLASTn GenBank NR

Note: "n"s represent regions that are not probed by the probe sequences.

Probe Sequence(5'-3')	Probe X	Probe Y	Probe Interrogation Position	Target Strandedness
CTACCGCTTGCCTATACACAGAGCGGTG	334	293	57	Antisense
GTGCCATACACAGAGCGTGCCTCTT	317	33	63	Antisense
AATGAACTATATCTGCAGCTCGATT	237	207	141	Antisense
TTCCAACTGAGATGAAGAGAGAAT	67	205	165	Antisense
CCACACTGACATGAAGGAGGAATCA	149	151	167	Antisense
GACATTGTCTTCATTTTCCAGTGT	184	77	192	Antisense
CTGCTGTGCTCATGACAGCGCGTG	349	129	225	Antisense
GTCGTCATGAACAGCGCGTTCAGTATG	181	529	231	Antisense
ATGAACAGCGCTGACTATGGGCGCT	96	325	237	Antisense
CTTGGAAGCAGAGGTGGAAATCCAA	26	227	259	Antisense
GGAAATCCAAAGACATGTCTTTCAG	533	157	275	Antisense
CTGCCAGTAATATCCAGGTAAATGG	220	353	333	Antisense
ACCTTTGACCATAGAAATCAAGCCTC	97	49	378	Antisense
GAATCAACCTTGAGCGCTGTGAGAT	501	41	391	Antisense
TGGAGACAGATATCTCCCTGACCAAT	15	507	426	Antisense
ATGTGAGCTATTTAAGAGATTAACC	341	19	454	Antisense

Sequence
Source

GenBank